
-continued

```

<210> SEQ ID NO 245
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic oligonucleotide"

<400> SEQUENCE: 245

```

gacaagaccc acacatgccc accttgtccg

30

```

<210> SEQ ID NO 246
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 246

```

Gly Thr Cys Pro Pro Cys Pro
1 5

```

<210> SEQ ID NO 247
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic oligonucleotide"

<400> SEQUENCE: 247

```

ggcacatgcc ctccatgtcc a

21

1. An antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (V_H) and a light chain immunoglobulin variable domain (V_L), wherein:

(a) the V_H comprises a V_H -CDR1 sequence of GVTFNYYG (SEQ ID NO: 3), a V_H -CDR2 sequence selected from the group consisting of ITRSGGRI (SEQ ID NO: 5) and ITSSGGRI (SEQ ID NO: 14), and a V_H -CDR3 sequence of TLDGRDGWVAY (SEQ ID NO: 4) or TLDGREGWVAY (SEQ ID NO: 156); and/or

(b) the V_L comprises a V_L -CDR1 sequence of: TGNIGSNY (SEQ ID NO: 7), a V_L -CDR2 sequence of RND (SEQ ID NO: 9), and a V_L -CDR3 sequence of: QSYS-SGFI (SEQ ID NO: 8).

2. An antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (V_H) and a light chain immunoglobulin variable domain (V_L), wherein:

(a) the V_H comprises a V_H -CDR1 sequence, a V_H -CDR2 sequence, and a V_H -CDR3 sequence of SEQ ID NO: 155, SEQ ID NO: 157, and SEQ ID NO: 156 respectively, and the V_L comprises a V_L -CDR1 sequence, a V_L -CDR2 sequence, and a V_L -CDR3 sequence of SEQ ID NO: 160, SEQ ID NO: 162, and SEQ ID NO: 161 respectively;

(b) the V_H comprises a V_H -CDR1 sequence, a V_H -CDR2 sequence, and a V_H -CDR3 sequence of SEQ ID NO: 115, SEQ ID NO: 117, and SEQ ID NO: 116 respectively, and the V_L comprises a V_L -CDR1 sequence, a V_L -CDR2 sequence, and a V_L -CDR3 sequence of SEQ ID NO: 120, SEQ ID NO: 122, and SEQ ID NO: 121 respectively;

(c) the V_H comprises a V_H -CDR1 sequence, a V_H -CDR2 sequence, and a V_H -CDR3 sequence of SEQ ID NO: 185, SEQ ID NO: 187, and SEQ ID NO: 186 respectively, and the V_L comprises a V_L -CDR1 sequence, a V_L -CDR2 sequence, and a V_L -CDR3 sequence of SEQ ID NO: 190, SEQ ID NO: 192, and SEQ ID NO: 191 respectively;

(d) the V_H comprises a V_H -CDR1 sequence, a V_H -CDR2 sequence, and a V_H -CDR3 sequence of SEQ ID NO: 135, SEQ ID NO: 137, and SEQ ID NO: 136 respectively, and the V_L comprises a V_L -CDR1 sequence, a V_L -CDR2 sequence, and a V_L -CDR3 sequence of SEQ ID NO: 140, SEQ ID NO: 142, and SEQ ID NO: 141 respectively;

(e) the V_H comprises a V_H -CDR1 sequence, a V_H -CDR2 sequence, and a V_H -CDR3 sequence of SEQ ID NO: 175, SEQ ID NO: 177, and SEQ ID NO: 176 respectively, and the V_L comprises a V_L -CDR1 sequence, a